

EXHIBIT 11



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

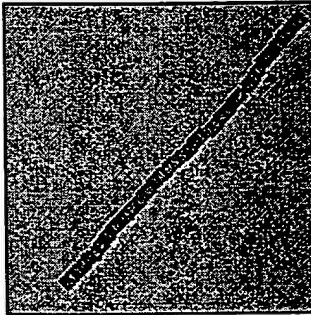
Sequence 1 lc|seq_1 Length 955 (1..955)

PMPE PTA 2462

Sequence 2 lc|seq_2 Length 839 (1..839)

POMP90B

2



1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 162 bits (411), Expect = 2e-38

Identities = 208/781 (26%), Positives = 329/781 (41%), Gaps = 114/781 (14%)

```

Query: 179 TFVVSSENQSCFLFMDNICIQTNTAGKGGAIYA-GTSNSFESNNCDLFFINNACCAGGAIF 237
          TF+ + CF DNI T TA GAI G + + LF + A C G
Sbjct: 85 TFLGNGYTLCF---DNI---TTTASNPGAINVQGGKTLGISGFSLF--SCAYCPPGTTG 136

Query: 238 SPICSLTGN-----RGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVT---GNRGRI 289
          GN ++VF+ KN TA +GGAI+ D N +
Sbjct: 137 YGAIQTKGNTTLKDNSSLVHF---KNCSTA---EGGAIQCKGSSDAELKIENNQN 186

Query: 290 FFSDNITKNYGGAIYAPVVTLVDNGPTYFINNVANN---KGGAIYI-DGTSNSKISADR 344
          FS+N + + GGAIYA +T+V GPT F NN +N KGGAI I D + ++AD
Sbjct: 187 VFSSENSSTSKGGAIYADKLTIVSGGPTLFSNNSVSNSSPKGGAISIKDSSGECSLTADL 246

Query: 345 HAIIFNENIVTNVTSANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSN 404
          I F+ N + + + T T RN+I + + L A + FYDPI
Sbjct: 247 GDITFDGNKIIKTSGSSSTVT-----RNSIDLGTGK-FTKLRAKDGFIFFYDPI TGGG 299

Query: 405 AG-VVSFNFKEADQTSVSVFSGATVNSAD-FHQRNLQTKTPAPLTLNGLFLCIEDHAQLT 462
          + ++++ + D TG +VPSG ++ + NL + P+TLS G L ++D +T
Sbjct: 300 SDELNINKKETVDYTGKIVFSGEKLSDEEKARAENLASTFNQIPITLSAGSLVLKDGVSVT 359

Query: 463 VNRFTQ-TGGVVSLSGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLV 521
          + TQ G V + G L +G +ITL ++ +N++S+ G
Sbjct: 360 AKQVTQEAGSTVVM DLGTTLQTPSSG-----GETITLTNLDINIASLGGGG-----T 407

Query: 522 EPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDLTHALSSQPMLSISEASDNQL 581
          P + N TA A T + ++L+D GN+ YE L +S+P +I ++
Sbjct: 408 SPAKLATN-TASQAITN---AVNLVDADGNA-YEDPILA---TSKPFTAIVATTNAST 458

Query: 582 RSDMDDFSGLNVP--HYGQGLWSWGWAQTQDPEPASSATITDPKANRFHRTLTLTLWLP 639
          + D VP HYG+QG W+ W D E A+ +T LTW
Sbjct: 459 VTQPTDNLNTNYVPPTHYGYQGNWTVW---DTETAT-----KTATLTWEQ 500

Query: 640 AGYVSPKHSPLIANTLWG--NMLLATESLKNSAELTPSDHPFWGITGGGLGMMVYQEP 697
          GY P+P+ + PL+ NTLWG + L A ++L + + H G GL +++
Sbjct: 501 TGYSNPNRQGPLVNTLWGAFSDLRAIQNLMDISVNGADYHR--GFWVSGLANFLHKSG 558

Query: 698 RENHPGFHMRSSGYFAGMIA--GQTHTFSLKFSQTYTKLNE-RYAKN--NVSSKNYSCQG 752

```

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DYGNSTPIESTULTHALSSQPMLSISEASDNQLRSDDMDPSGLNVPHYGWQLWSWGNAKIY
DPEPASSATITDPKKNRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHFPWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPPFGSTHILTAPFLGALGIYSSLSHFTVEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQFVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHPQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ITINAVNLVDALGNATEDFILATSKPFTAI VATINASTVITQPTDNLNTNIVFPFTHGYQGN
WTVTWDTETATKTATLTWEQTYSPNPERQGPLVPNTLWGAFSDLRAIQNLMDISVNGAD
YHRGFVWVSGLANFLHKSGSDTKRKFHNSAGYALGVYAKTPSDDIFSAAFQQLFGKDKDY
LVSKNNANIYAGSLYYQHSYWSAWQNLQNTIGAEAPLVLNAQLTYCHASNDMKTMTT
TYAPRKTTYAEIKGDWGNDCFGVELGATVPIQTESSLLFDMYSPFLKFQLVHTHQDDFKE
NNSDQGRYFESSNLTNLSLPIGIKFERFANNDTASYHVTAAYS PDIVRSNPDCTTSLLV
PDSAVWVTKANNLARSAPMLQAGNYLSLSHNIEIFSQGFELRGSSRTYNVDLGSKIQF
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

+ F S+GY G+ A FS F Q + K + +KN N+ + + Q
Sbjct: 559 SDTKRKRFRHNSAGYALGVYAKTPSDDIFSAAFQCQLFGKDKDYLVSKNNANIYAGSLYYQH 618

Query: 753 EMLFSLQEGFLLAKLVGLYSYGDHN-----CHHFTYQGENLTS-----QGTFR 795
 +S + LL +G + N CH N+T+ +G +
Sbjct: 619 ISYWSAWQN-LLQNTIGAEAPLVLNAQLTYCHASNDMKTNTTITYAPRKTTYAEIKGDWG 677

Query: 796 SQTMGGAFFDLEPMKPGSTHI-LTAPFLGALGIYSSLSHFTEVGAYPRSPSTKTPLINV 854
 + G + +P++ S + PFL +++ F E + + + L N+
Sbjct: 678 NDCFGVELGATVPIQTESSLLFDMYSPFLKFQLVHTHQDDPKENNSDQGRYFESSNLNL 737

Query: 855 LVPIGVKGSFMNATORPQAWTVELAYQFVLYRQELEIATQLLAS--KGIWFGSGSPSSRH 912
 +PIG+K A ++ V AY P + R + T L L S +W + +R
Sbjct: 738 SLPIGKIFERF-ANNDTASYHVTAAYSPDIVRSNPDCTTSLLVSPDSAVVWTKANNLARS 796

Query: 913 A 913
 A
Sbjct: 797 A 797

CPU time: 0.22 user secs. 0.03 sys. secs 0.25 total secs.

Lambda	K	H
0.316	0.132	0.396

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9570

Number of Sequences: 0

Number of extensions: 806

Number of successful extensions: 12

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 955

length of database: 326,887,585

effective HSP length: 133

effective length of query: 822

effective length of database: 281,363,015

effective search space: 231280398330

effective search space used: 231280398330

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from **NCBI ftp site**.
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gap x_dropoff expect word size Filter ☒

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or sequence in FASTA format from: to:

```
DTGNSPTSTLTHALSSQPLSLISEASUNQLKSDUMUFGSLNVPHYGWQLLWSWGWAQIQ  
DPEPASSATITDPKANKRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERVAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTOGENLTSQGT  
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGELALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
HIGYQGNWTVTWKQSSAQKRTATLTWEQITGYSFNFERQSSLVFNTLWGSFSDIRAIQNL  
MDISVNGADYHRGFVWVSLGNFLHKSGSDTKRFRHNSAGYALGVYAQTSPSEDFVSA AFC  
QLFGKDKDYLVSKNSSSTVYAGSIYYQHISYWNWNTLLQNTLGAEAPLVNLAQLAYCHAS  
NNMKTMTDTYAPPKTTYSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPPVKLQLVH  
AHQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKPSHKDTASYNLTAYAPDIVRSNPD  
CTASLLVSPTS AVWVTKANLARHAFILQAGNYLALTRNTELSQFGFELRGSCRTYNID  
LGSKIQF
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

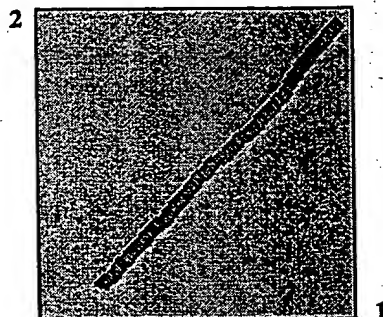


Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq_1 Length 955 (1..955) **PMPE PTA 2462**
 Sequence 2 lc|seq_2 Length 847 (1..847) **POMP 91 A**



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 174 bits (441), Expect = 7e-42
 Identities = 196/767 (25%), Positives = 318/767 (40%), Gaps = 101/767 (13%)

```

Query: 190 LFMENICIQNTNAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGN--- 246
          L DNI  T ++ G  +GT+ + + + LF + A C GA          GN
Sbjct: 97 LCFDNIT--TQSSHPGAISVSGTNKTLDISGFSLF--SCAYCPPGATGYGAIKAVGNTTI 152

Query: 247 --RGNIVFYNNRCFKNVETASSEASDGGAIKVTTRL DVTGNRGRIFSDNITKNYGGAIY 304
          ++VF+  KN T A A L + N+ +F ++N + + GGAIY
Sbjct: 153 KDNSSLVFH-----KNCSTGEGGAIQCKASSSEAELKIENNQLVLF-AENSSSSSGGAIY 206

Query: 305 APVVTLV DNGPTYFINN---VANNKGGAIYI-DGTSNSKISADRHAIIFNENIVTNVTS A 360
          A +T+V GPT F NN ++ KGGAI I D ++AD I F+ N +
Sbjct: 207 ADKLTIVSGGPTLFSNNVSASSPKGGAICIKDSGGECSLTADLGDTTFDGNKI IKTNGG 266

Query: 361 NGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNA GVSVSFNKE--ADQT 418
          + T T RN+I + SS L A + FYDPI ++ NK+ D T
Sbjct: 267 SPTVT-----RNSIDLSSGKPTKLNAGEFGFIFFYDPI-TGGGSDELNINKQD TVDYT 319

Query: 419 GSVVFSGATVNSADFH-QRNLTQKTPAPLTL SNGFLCIEDHAQLTVNRFTQT-GGVVSLG 476
          G +VFSG ++ + NL++ PL + +G L ++D L FTQT G V +
Sbjct: 320 GKIVFSGERLSDEEKVAANLKSDFKQPLKIGSGSLILKDGVTLETQSFTQTEGATV VMD 379

Query: 477 NGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAA 536
          G L +G +ITL ++ +N++S+ G VE T S T +
Sbjct: 380 LGTTLTQTSSGG-----ETITLTNLDINVASLGGGVAPDPAKVEATTESKTVTINA-- 431

Query: 537 TFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSIS--EASDNQLRSDDMDFSGLNVP 594
          ++L+DD GN+ YE L +SQP +I S + + P
Sbjct: 432 -----VNLVDNNGNA- YEYPI LA---ASQPFTAIEVRSGSSGSITKPTTNLENYTPP 479

Query: 595 -HYGWQGLWSWGWAQTQDPEPASSATITDPKKANRPHRTL LTLWLPAGYVPSPKHRSPLI 653
          HYG+QG W+ W + SSA +T LTW GY P+P+ + L+
Sbjct: 480 THYGYQGNWTVTWKQ-----GSSAQ-----EKTATLTWEQTGYSPNPERQGS LV 523

Query: 654 ANTLWGNMLLATESLKNASAE LTPSDHPFW-GITGGGLGMMVYQEPRENHPGFHRSSGYF 712
          NTLWG+ +++N +++ + + G GLG +++ + F S+GY
Sbjct: 524 PNTLWGS-PSDIRAIQNLMDISVNGADYHRGFVWSGLGNFLHKS GSDTKRKFRHNSAGYA 582

Query: 713 AGMIA--GQTHTFSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLF-----SLQE 760
  
```

G+ A FS F Q + K ++ Y + SS Y+ G + + +L +
 Sbjct: 583 LGVYAQTSEDVFSAAFQQLFGK-DKDYLVSKNSSTVYA--GSIYYQHISYWNNTWNTLLQ 639

Query: 761 GFLAKLVGLYSYGDHNCCHFYTQGENLTS-----QGTFRSQTMGGAVFFDLP 808
 L A+ + CH N+T +G + + G P
 Sbjct: 640 NTLGAEAPLVLNAQLAYCHASNMMKTNTMDTYAPPKTTYSEIKGDWGNDCFGVEFGAKAP 699

Query: 809 MKPFGSTHILTAPFLGALGIYSSLSHFTVEVGAYPRSFSTKTPLINVLVPIGVKGSFMNAT 868
 ++ + +PF+ +++ F E + + L N+ +PIGVK +
 Sbjct: 700 IETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKF-SH 758

Query: 869 QRPQAWTVELAYQPVLRYQELEIATQLLAS--XGIWFGSGSPSSRHA 913
 + ++ + LAY P + R + LL S +W + +RHA
 Sbjct: 759 KDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSASVWVTKANNLARHA 805

CPU time: 0.23 user secs. 0.03 sys. secs 0.26 total secs.

Lambda K H
 0.316 0.132 0.396

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 10,082

Number of Sequences: 0

Number of extensions: 843

Number of successful extensions: 16

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 955

length of database: 326,887,585

effective HSP length: 133

effective length of query: 822

effective length of database: 281,363,015

effective search space: 231280398330

effective search space used: 231280398330

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

BLAST 2 SEQUENCES

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Open gap and extension gap penalties

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```
DYGNSTFESTDTHALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGWQGLWSGWAKIV  
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKN  
AELTPSDHPPFWGITGGGLGMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMKFFGSTHILTAPFLGALGIYSSLSHFTVEVGAYPRSFSTKTPLIN  
LVPIGVKGSFPMNATQRPQAWTVELAYQFVLYRQELEIATQLLASKGIWFGSGSPSSRHMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DISVNGADYSRGFWSSLANFLNAGSUTRRKFRHRSAGYALGVYAQTFSDDVCSAAFCV  
LFGKDKDYFVSKNSSTIYAGSIYYQHISYWNWNTLLQNTLGAEAPLVLNAQLTYCHASN  
NMKTNMTNTYTPKNVTPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPFVKLQLVHA  
HQDDFKENNNDQGRYPESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPDC  
TASLLVSPTSAAVWVTKANNLARHAFILQAGNYLALTRNTELSQFGFELRGSCRTYNIDL  
GSKIQF
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

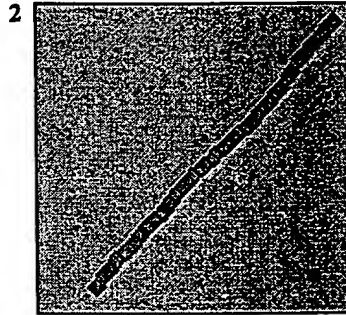


Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq_1 Length 955 (1..955) *PMP E PTA 2462*
 Sequence 2 lc|seq_2 Length 846 (1..846) *Pomp 91 B*



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 162 bits (409), Expect = 4e-38
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```

Query: 172 GAISTANTFVVSSENQSCFLFMDN---IC---IQTNITAGKGGAIYAGTSNSFESNCDLFF 225
          G S N SE F+ N +C I T ++ G +GT+ + + + LF
Sbjct: 68 GKDSPLNKSCFSETTENLSFGNGYTLFCFDNITTQSSHGAISVSGTNKTLDISGFSLFS 127

Query: 226 INNACCAG---GAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTRLD 281
          C G GAI + + + ++VF+ KN TA A + T L
Sbjct: 128 CAYCCPPGTTGYGAIQTKGTTTLKDNSSLVFH-----KNCSTAEGGAIQCKSSSSTAELK 182

Query: 282 VTGNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN-VANN---KGGAIYI-DGTS 336
          + N+ +F S+N +K GGAIYA +T+V GPT F NN V++N KGGAI I D
Sbjct: 183 LENNKLVF-SENSSKEKGGAIYADKLTIIVSGGPTLFSNNSVSHNSSPKGGAICIKDSG 241

Query: 337 NSKISADRHAIIFNENIVTNVTSANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLP 396
          ++A+ I F+ N + + T T RN+I + S L A + F
Sbjct: 242 ECSLTANLGDITFDGNKIITNGGSPTVT-----RNSIDLGGGKFTKLNAGEFGIF 295

Query: 397 YDPIEVSNAGVSVSFNK---EADQTSVVFSGATVNSAD-FHQRNLQTKTPAPLTLNNGF 452
          YDPI + + NK + TG +VFSG ++ + NL++ PL + G
Sbjct: 296 YDPIANTGGSTEIELNKTESDTTYTGKIVFSGEKLSDDEKTVPANLKSYPKQPLKIGAGS 355

Query: 453 LCIEDHAQLTVNRFTQT-GGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILK 511
          L ++D L + TQT G V + G L S+S +ITL ++ +N++S+
Sbjct: 356 LVLKDGVTLEAKKITQTKGSTVMDLGTTLQT-----PSSSGETITLTNLDINIASLGG 409

Query: 512 SGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKLSLIDYGNSPYESTDLTHALSSQPML 571
          G P A A+ ++S ++L++ N+ YE L+ + S +
Sbjct: 410 GGGTAPA-----KLATNTASQAISIAAVNLVNTDSNT-YEDPILSASKSFSAIT 457

Query: 572 SISEASDNQLRSDMDPFGSLNVP-HYGWQGLWSGWAKTQDPEPASSATITDPKKANRPH 630
          + + S + + + + P HYG+QG W+ W + SSA
Sbjct: 458 ATT--SSSTVTPPETNLKNYTPPTHYGYQGNWTVTW-----KQGSSAQ-----E 499

Query: 631 RTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPPF-WGITGGGL 689
          +T LTW GY P+P+ L+ NTLWG T +++N +++ + + G L
Sbjct: 500 KTATLTWEQTGYSNPFRVGSGLVPNTLWG-AFSDTRAIONLMDISVNGADYSRGFWVSS 558

Query: 690 GMMVYQEPRENHPGFHMRSSGYFAGMIA--GQTHTPSLKFSQTYTKLNERYAKNNVSSKN 747
  
```

```

      + + +   F   S+GY G+ A       S F Q + K + +   N S S
Sbjct: 559 ANFLNKSGSDTKRKFRHHSAGYALGVYAQTTPSDDVCSAAFCQLFGKDKDYFVSKN-SSTI 617

Query: 748 YSCQGEMLF-----SLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTS----- 790
      Y+ G + +       +L + L A+ + +       CH       N+T+
Sbjct: 618 YA--GSIYYQHISYWNWNTLLQNTLGAEAPLVNAQLTYCHASNMMKTMNTNTYTPKNV 675

Query: 791 -----QGTFRSQTMGGAFFDLPMKFPFGSTHILTAFFLGALGIYSSLSHFTEVGAYPRSF 845
      +G + + G       P++       + +PF+       +++       F E + +
Sbjct: 676 TPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRY 735

Query: 846 STKTPLINLVPIGVKGSFMNATQRPQAWTVELAYQPVLVYRQELEIATQLLAS--KGIWF 903
      L N+ +PIGVK       + +   ++ + LAY P + R +       LL S   +W
Sbjct: 736 FESNNLTNLSMPIGVKLEKF-SHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSAVWV 794

Query: 904 GSGSPSSRHA 913
      + +RHA
Sbjct: 795 TKANNLARHA 804

```

CPU time: 0.23 user secs. 0.03 sys. secs 0.26 total secs.

Lambda K H
0.316 0.132 0.396

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

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effective search space: 231280398330

effective search space used: 231280398330

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)